LOCUS Extrémité C-terminale récepteur AT2 160 BP DS-DNA

ORGANISM Souris
BASES 41 A 33 C 36 G 50 T

ac.nucléiques 1 TGTGTTAATC CCTTCCTGTA TTGTTTTGTT GGAAACCGCT
TCCAACAGAA CGTCCGCAGT GTGTTTAGAG TTCCCATTAC
TTGGCTCCAA GGCAAGAGAG AGACTATGTC TTGCAGAAAA
121 GGCAGTTCTC TTAGAGAAAT GGACACCTTT GTGTCTTAAA

Traduction en acides aminés

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GSSLREMDTFVS•

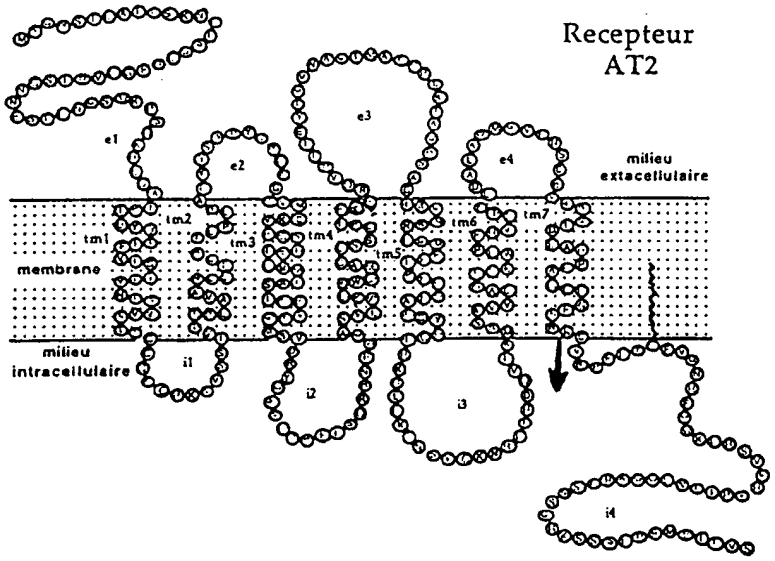
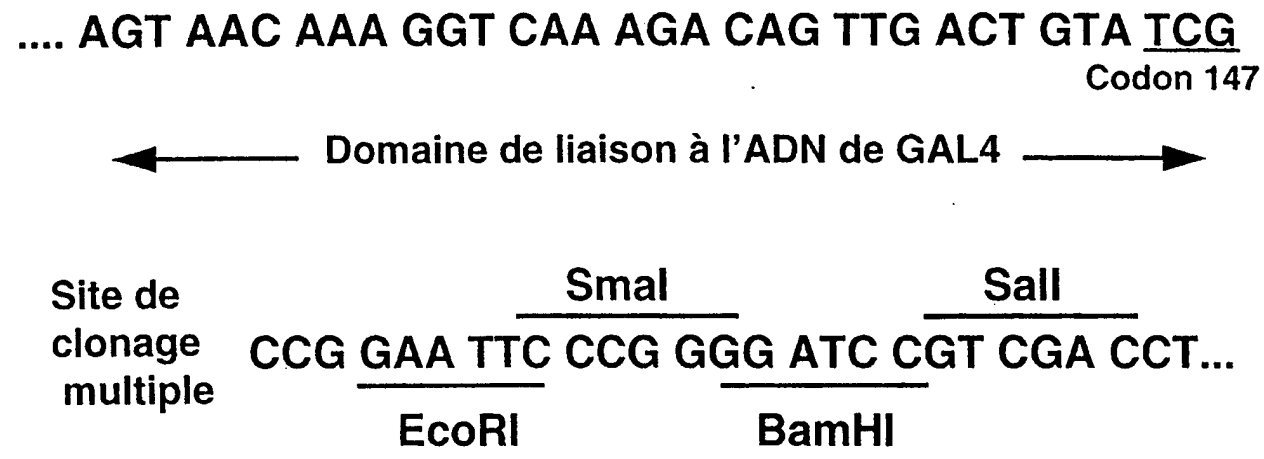


Figure 1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Codon 147
Domaine de liaison à l'ADN de GAL4
Site de clonage multiple
SmaI
SalI
CCG GAA TTC CCG GGG ATC CGT CGA CCT...
EcoRI
BamHI

Figure 2

```
GCTACCCCCCCCCCCACGCACCCCCCAATCTGGGTGGCCTGGCATTAGCATGTAAGCTTGTTTTTCTCTGGC    71

TGTATCTCTTGGCCTGGAAGAACCCCGAGTTGCCAAGAGACACAGTATGTGATGGTCCCTGGAAAAGCTGCT   143

                                        M   L   L   S   P   K   F   S   L       9
TCCCCTGCGAAGTTCTCCCACTGGCTTCGAAGAC ATG CTG TTG TCT CCC AAA TTC TCC TTA       204

 S   T   I   H   V   R   L   T   A   K   G   L   L   R   N   L   R   L      27
TCC ACC ATC CAC GTC CGC CTA ACC GCC AAA GGA CTG CTT CGA AAC CTC CGG CTT      258

 P   S   G   L   R   K   N   T   V   I   F   H   T   V   E   K   G   R      45
CCT TCG GGG CTC AGG AAA AAC ACT GTC ATT TTC CAC ACA GTT GAA AAG GGC AGG      312

 Q   K   N   P   R   S   L   C   I   Q   T   Q   T   A   P   D   V   L      63
CAG AAG AAT CCC AGG AGC CTG TGC ATC CAG ACC CAG ACA GCT CCA GAT GTG CTG      366

 S   S   E   R   T   L   E   L   A   Q   Y   K   T   K   C   E   S   Q      81
TCC TCC GAG AGA ACG CTT GAG TTG GCC CAA TAC AAG ACA AAA TGT GAA AGC CAA      420

 S   G   F   I   L   H   L   R   Q   L   L   S   R   G   N   N   K   F      99
AGT GGA TTC ATC CTG CAC CTC AGG CAG CTT CTT TCC CGT GGT AAC AAC AAG TTT      474

 E   A   L   T   V   V   I   Q   H   L   L   S   E   R   E   E   A   L     117
GAA GCG CTG ACA GTT GTG ATC CAG CAC CTC CTG TCT GAG CGG GAG GAA GCA CTG      528

 K   Q   H   K   T   L   S   Q   E   L   V   S   L   R   G   E   L   V     135
AAG CAA CAC AAA ACC CTC TCT CAA GAA CTT GTC AGC CTC CGG GGA GAG CTA GTT      582

 A   A   S   S   A   C   E   K   L   E   K   A   R   A   D   L   Q   T     153
GCT GCT TCA AGC GCC TGT GAG AAG CTA GAA AAG GCT AGG GCT GAC TTA CAG ACA      636

 A   Y   Q   E   F   V   Q   K   L   N   Q   Q   H   Q   T   D   R   T     171
GCG TAT CAA GAA TTT GTC CAG AAA CTA AAC CAG CAG CAT CAG ACA GAC CGG ACG      690

 E   L   E   N   R   L   K   D   L   Y   T   A   E   C   E   K   L   Q     189
GAA CTG GAG AAC CGG CTG AAG GAC TTA TAC ACC GCA GAG TGT GAG AAG CTT CAG      744

 S   I   Y   I   E   E   A   E   K   Y   K   T   Q   L   Q   E   Q   F     207
AGC ATT TAC ATT GAG GAG GCA GAA AAA TAT AAA ACT CAA CTG CAA GAG CAG TTT      798

 D   N   L   N   A   A   H   E   T   T   K   L   E   I   E   A   S   H     225
GAC AAC TTA AAC GCC GCC CAT GAG ACC ACT AAG CTT GAG ATT GAA GCT AGC CAC      852

 S   E   K   V   E   L   L   K   K   T   Y   E   T   S   L   S   E   I     243
TCG GAG AAG GTG GAA TTG CTG AAG AAG ACC TAT GAA ACC TCC CTT TCA GAA ATC      906

 K   K   S   H   E   M   E   K   K   S   L   E   D   L   L   N   E   K     261
AAG AAG AGC CAT GAG ATG GAG AAG AAG TCA CTG GAG GAT CTG CTT AAT GAG AAG      960

 Q   E   S   L   E   K   Q   I   N   D   L   K   S   E   N   D   A   L     279
CAG GAA TCG CTG GAG AAA CAA ATC AAT GAT CTG AAG AGT GAA AAC GAT GCT TTA     1014

 N   E   R   L   K   S   E   E   Q   K   Q   L   S   R   E   K   A   N     297
AAC GAA AGG TTG AAA TCA GAG GAG CAA AAG CAA CTG TCA AGA GAG AAG GCG AAT     1068

 S   K   N   P   Q   V   M   Y   L   E   Q   E   L   E   S   L   K   A     315
TCC AAA AAC CCT CAG GTC ATG TAT CTG GAG CAA GAA CTA GAA AGC CTG AAG GCT     1122
```

1 2 3

Figure 3.1

```
V   L   E   I   K   N   E   K   L   H   Q   Q   D   M   K   L   M   K    333
GTG TTA GAG ATC AAG AAT GAG AAG CTG CAC CAG CAG GAC ATG AAG CTA ATG AAG  1176

M   E   K   L   V   D   N   N   T   A   L   V   D   K   L   K   R   F    351
ATG GAA AAG CTG GTG GAC AAT AAC ACA GCA TTG GTT GAC AAG CTG AAG CGA TTC  1230

Q   Q   E   N   E   E   L   K   A   R   M   D   K   H   M   A   I   S    369
CAG CAG GAA AAC GAG GAG TTA AAA GCT CGC ATG GAC AAA CAC ATG GCA ATT TCA  1284

R   Q   L   S   T   E   Q   A   A   L   Q   E   S   L   E   K   E   S    387
AGG CAA CTT TCC ACC GAG CAG GCC GCG CTG CAA GAG TCC CTT GAG AAG GAG TCA  1338

K   V   N   K   R   L   S   M   E   N   E   E   L   L   W   K   L   H    405
AAG GTC AAC AAG AGA CTG TCC ATG GAG AAC GAG GAA CTT CTG TGG AAA CTG CAC  1392

N   G   D   L   C   S   P   K   R   S   P   T   S   S   A   I   P   F    423
AAC GGA GAC CTG TGC AGC CCC AAG AGA TCC CCC ACC TCC TCG GCC ATC CCT TTC  1446

Q   S   P   R   N   S   G   S   F   S   S   P   S   I   S   P   R   *    440
CAG TCC CCC AGG AAT TCT GGT TCC TTC TCC AGC CCC AGC ATC TCA CCC AGA TGA  1500

CGGCTTCTGAACGCAGGAGACTCTCTGAAGGCACTGAGGTGCGCTTCTGCAGGACTGACCCTCTCATGGGA  1571

ACTCGAGTTGCTGCGTTAGCTCTCTGGAATATCCCCAGGATATCGGGAGAGCAGCCGCCAACCGTATCAGC  1642

TACGTACGAATAGAGAGCTCCAATAGAAGACTTTTAACTTGGTCCAAAAGCCTCCTCCAAAAACAGATTTC  1713

GGAACTGAAGTGGACATAGTTGCACAAAGCACTTACGGAACGAGGGAACCTTGTTCTTTGCCTTCCTTCAC  1784

CTAAGCATAGGCTTTCCAG                                                      1803
```

4

Figure 3.2

```
cagtgtgatgtggttcagaggcagcttctagacctgcaggagggagattgtattcagaggaagagcatcatt   72

ttggcaacatctgaaagtgaaaacggaagccagaaacacttggccagccctgggggatttttttcttctatg  144

cctctgtggtggaatgacatttgctgtgtaggcatctttcctctgactgtatttcttggccttgaagagtac  216

tgagtttaaaaagacagtatgtgacagtccatggaaattgcctcttctgtgaaatctcgccacctgctccga  288

agac ATG TTG TTG TCT CCC AAA TTC TCC TTA TCC ACC ATT CAC ATA CGA CTG ACG  343
     M   L   L   S   P   K   F   S   L   S   T   I   H   I   R   L   T   17

GCC AAA GGA TTG CTT CGA AAC CTT CGA CTT CCT TCA GGG TTT AGG AGA AGC ACT  397
 A   K   G   L   L   R   N   L   R   L   P   S   G   F   R   R   S   T   35

GTT GTT TTC CAC ACA GTT GAA AAG AGC AGG CAA AAG AAT CCT CGA AGC TTA TGT  451
 V   V   F   H   T   V   E   K   S   R   Q   K   N   P   R   S   L   C   53

ATC CAG CCA CAG ACA GCT CCC GAT GCG CTG CCC CCT GAG AAA ACA CTT GAA TTG  505
 I   Q   P   Q   T   A   P   D   A   L   P   P   E   K   T   L   E   L   71

ACG CAA TAT AAA ACA AAA TGT GAA AAC CAA AGT GGA TTT ATC CTG CAG CTC AAG  559
 T   Q   Y   K   T   K   C   E   N   Q   S   G   F   I   L   Q   L   K   89

CAG CTT CTT GCC TGT GGT AAT ACC AAG TTT GAG GCA TTG ACA GTT GTG ATT CAG  613
 Q   L   L   A   C   G   N   T   K   F   E   A   L   T   V   V   I   Q  107

CAC CTG CTG TCT GAG CGG GAG GAA GCA CTG AAA CAA CAC AAA ACC CTA TCT CAA  667
 H   L   L   S   E   R   E   E   A   L   K   Q   H   K   T   L   S   Q  125

1 GAA CTT GTT AAC CTC CGG GGA GAG CTA GTC ACT GCT TCA ACC ACC TGT GAG AAA  721
   E   L   V   N   L   R   G   E   L   V   T   A   S   T   T   C   E   K  143

TTA GAA AAA GCC AGG AAT GAG TTA CAA ACA GTG TAT GAA GCA TTC GTC CAG CAG  775
 L   E   K   A   R   N   E   L   Q   T   V   Y   E   A   F   V   Q   Q  161

CAC CAG GCT GAA AAA ACA GAA CGA GAG AAT CGG CTT AAA GAG TTT TAC ACC AGG  829
 H   Q   A   E   K   T   E   R   E   N   R   L   K   E   F   Y   T   R  179

GAG TAT GAA AAG CTT CGG GAC ACT TAC ATT GAA GAA GCA GAG AAG TAC AAA ATG  883
 E   Y   E   K   L   R   D   T   Y   I   E   E   A   E   K   Y   K   M  197

CAA TTG CAA GAG CAG TTT GAC AAC TTA AAT GCG CAT GAA ACC TCT AAG TTG GAA  937
 Q   L   Q   E   Q   F   D   N   L   N   A   H   E   T   S   K   L   E  215

2 ATT GAA GCT AGC CAC TCA GAG AAA CTT GAA TTG CTA AAG AAG GCC TAT GAA GCC  991
   I   E   A   S   H   S   E   K   L   E   L   L   K   K   A   Y   E   A  233

TCC CTT TCA GAA ATT AAG AAA GGC CAT GAA ATA GAA AAG AAA TCG CTT GAA GAT 1045
 S   L   S   E   I   K   K   G   H   E   I   E   K   K   S   L   E   D  251

TTA CTT TCT GAG AAG CAG GAA TCG CTA GAG AAG CAA ATC AAT GAT CTG AAG AGT 1099
 L   L   S   E   K   Q   E   S   L   E   K   Q   I   N   D   L   K   S  269

3 GAA AAT GAT GCT TTA AAT GAA AAA TTG AAA TCA GAA GAA CAA AAA AGA AGA GCA 1153
   E   N   D   A   L   N   E   K   L   K   S   E   E   Q   K   R   R   A  287

AGA GAA AAA GCA AAT TTG AAA AAT CCT CAG ATC ATG TAT CTA GAA CAG GAG TTA 1207
 R   E   K   A   N   L   K   N   P   Q   I   M   Y   L   E   Q   E   L  305
```

Figure 4.1

```
GAA AGC CTG AAA GCT GTG TTA GAG ATC AAG AAT GAG AAA CTG CAT CAA CAG GAC  1261
 E   S   L   K   A   V   L   E   I   K   N   E   K   L   H   Q   Q   D    323

ATC AAG TTA ATG AAA ATG GAG AAA CTG GTG GAC AAC AAC ACA GCA TTG GTT GAC  1315
 I   K   L   M   K   M   E   K   L   V   D   N   N   T   A   L   V   D    341

AAA TTG AAG CGT TTC CAG CAG GAG AAT GAA GAA TTG AAA GCT CGG ATG GAC AAG  1369
 K   L   K   R   F   Q   Q   E   N   E   E   L   K   A   R   M   D   K    359

CAC ATG GCA ATC TCA AGG CAG CTT TCC ACG GAG CAG GCT GTT CTG CAA GAG TCG  1423
 H   M   A   I   S   R   Q   L   S   T   E   Q   A   V   L   Q   E   S    377

CTG GAG AAG GAG TCG AAA GTC AAC AAG CGA CTC TCT ATG GAA AAC GAG GAG CTT  1477
 L   E   K   E   S   K   V   N   K   R   L   S   M   E   N   E   E   L    395

CTG TGG AAA CTG CAC AAT GGG GAC CTG TGT AGC CCC AAG AGA TCC CCC ACA TCC  1531
 L   W   K   L   H   N   G   D   L   C   S   P   K   R   S   P   T   S    413

TCC GCC ATC CCT TTG CAG TCA CCA AGG AAT TCG GGC TCC TTC CCT AGC CCC AGC  1585
 S   A   I   P   L   Q   S   P   R   N   S   G   S   F   P   S   P   S    431

ATT TCA CCC AGA TGA  cacgtccccaaagtccacagactctctgaaagcattttgatgcaggtctgc  1651
 I   S   P   R   *                                                        436

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Figure 4.2

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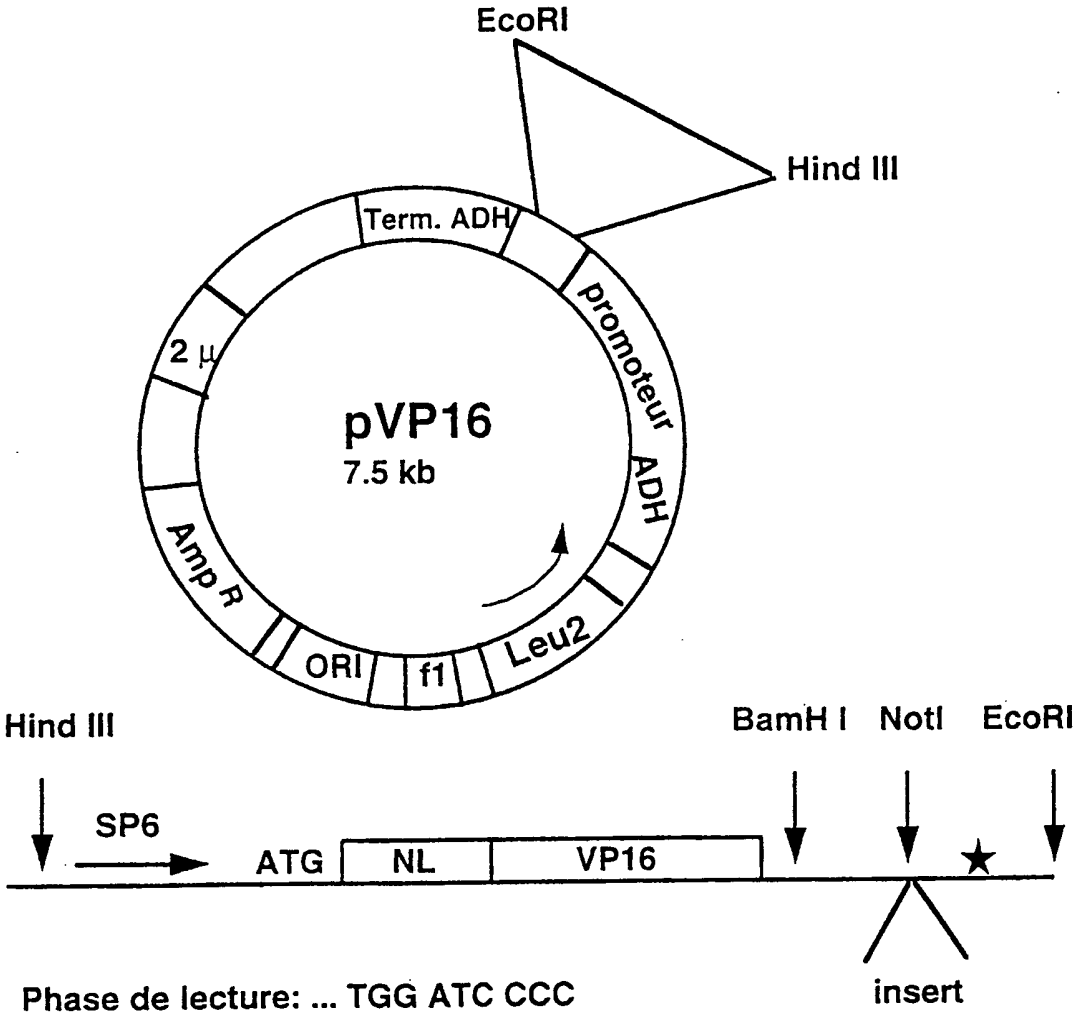
Figure 4.3



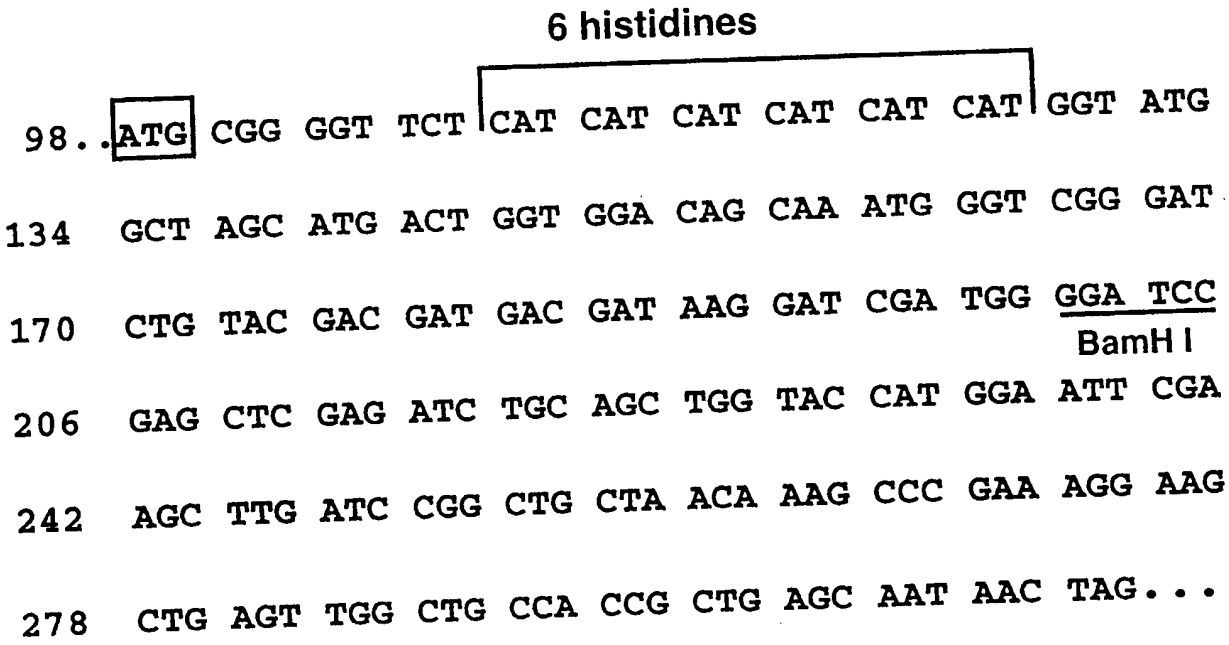
Phase de lecture: ... TGG ATC CCC

BamHI

★ codons de terminaison dans trois phases

pVP16 a été construit par Stan Hollenberg

Figure 5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BamH I
206 GAG CTC GAG ATC TGC AGC TGG TAC CAT GGA ATT CGA
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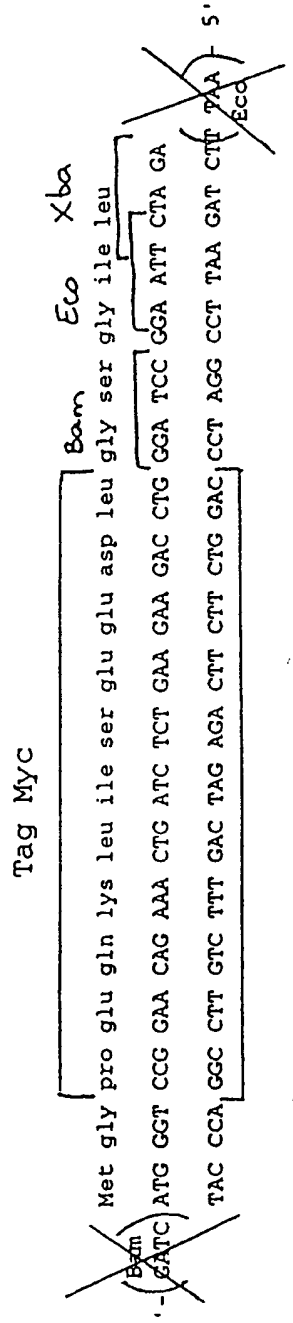
Figure 6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Bam
Eco
Xba
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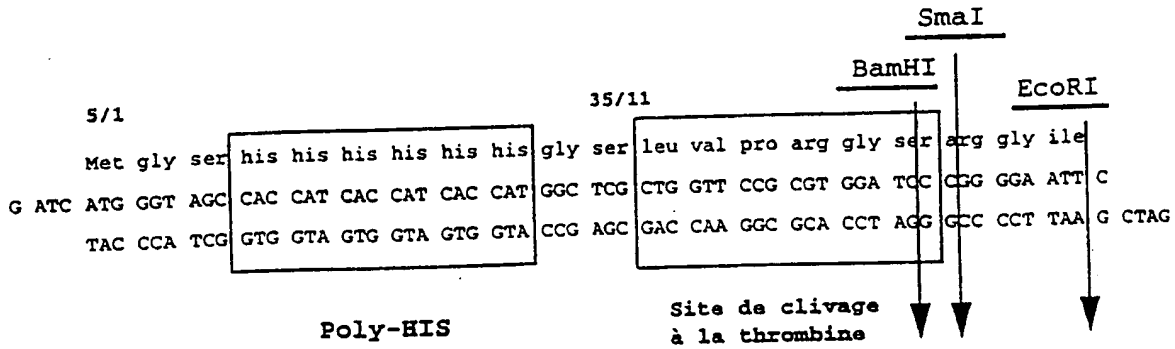
5'
Bam
GATC
Eco
5'

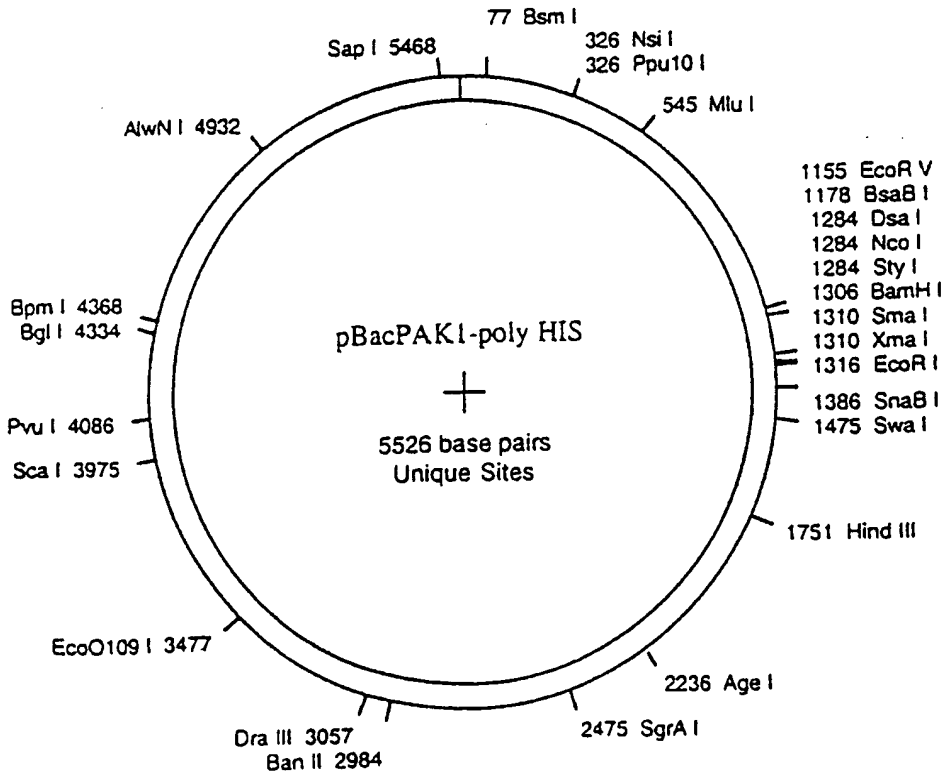
Figure 7



pBacPAK1-poly HIS -> Graphic Map

DNA sequence 5526 b.p. AACGGCTCCGCC ... TCATTAATGCAG circular

insertion polyHIS dans pBacpack en BamHI (CACCAT)3 1270-1287



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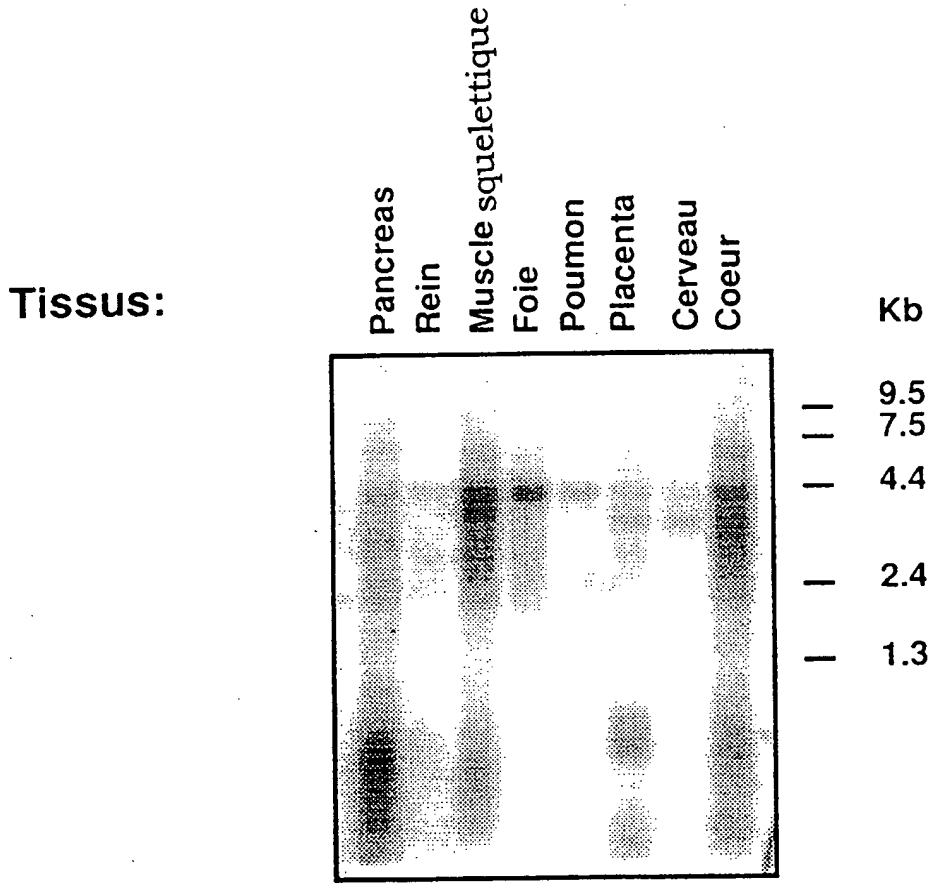
Tissus:
Pancreas
Rein
Muscle squelettique
Foie
Poumon
Placenta
Cerveau
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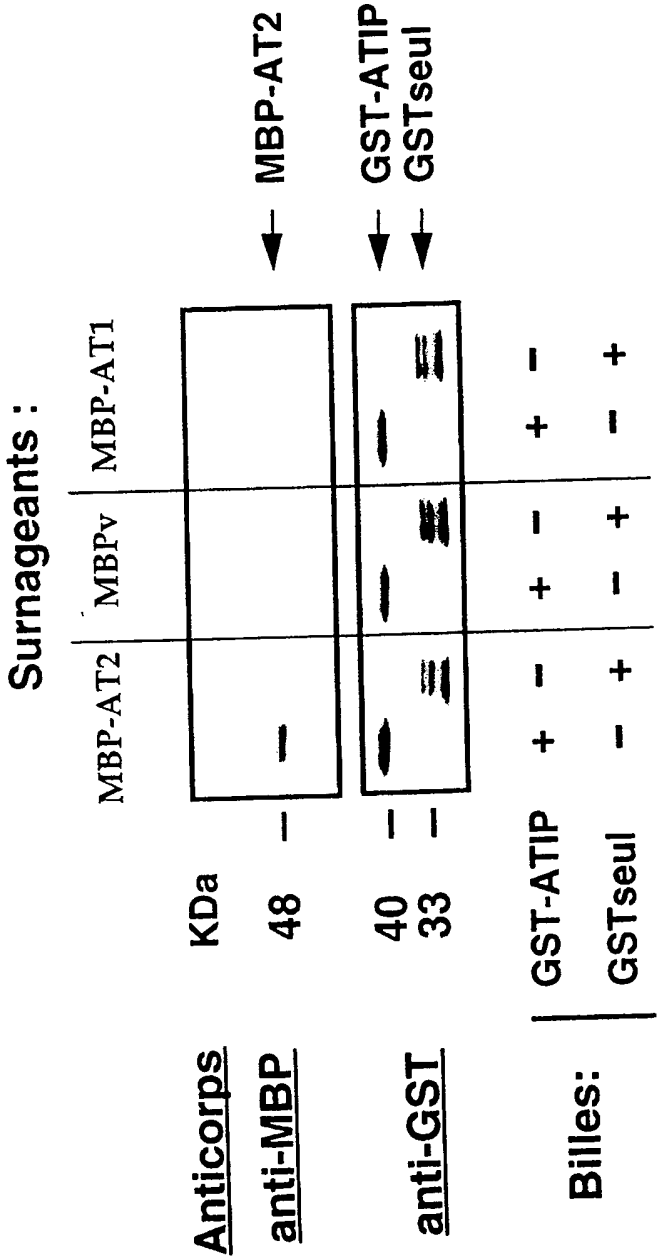
Kb
9.5
7.5
4.4
2.4
1.3

Figure 9


Surnageants :
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40
33
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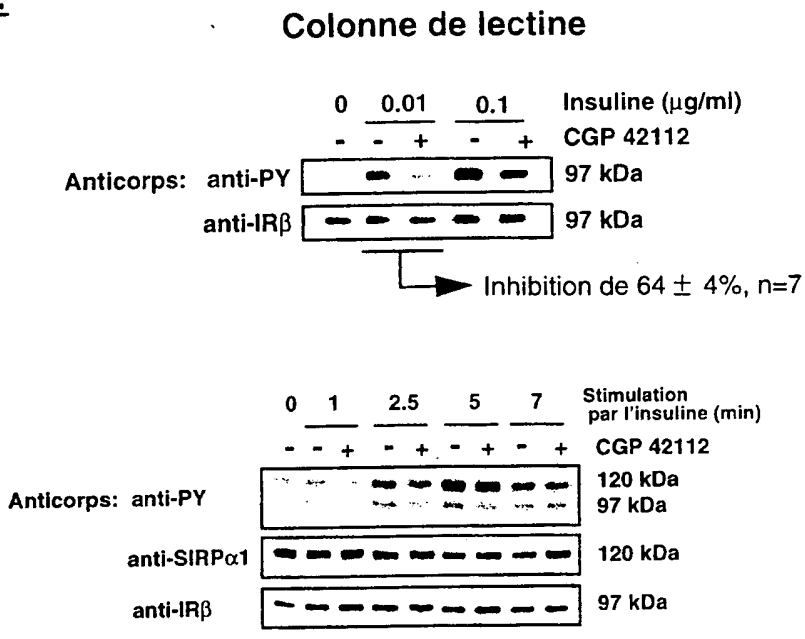
Figure 10

CHO-hAT2



CHO-hAT2 et CHO-hAT2-ATIP

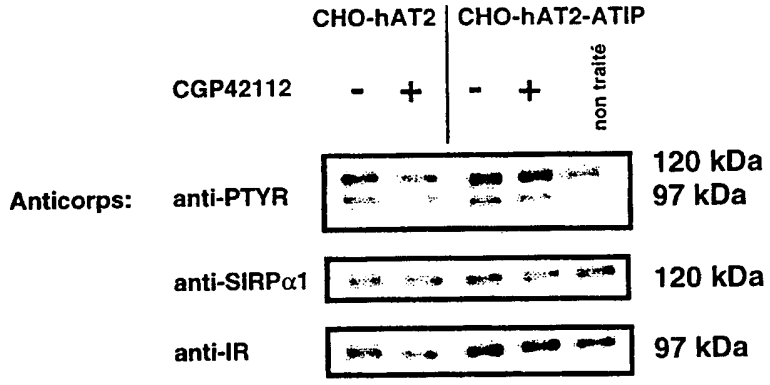


Figure 11